

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 10:30:26 ; Search time 25.2 Seconds

(without alignments)
34,318 Million cell updates/sec

Title: 09-403627-1
Perfect score: 45
Sequence: 1 avd1shf1k 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 788

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR-71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	37.8	9	2	S07205
2	17	37.8	9	2	S07204
3	16	35.6	9	2	S07241
4	16	35.6	9	2	D48186
5	15	33.3	8	2	PC4131
6	15	33.3	9	2	JN0026
7	14	31.1	5	4	A58728
8	14	31.1	7	2	S20446
9	14	31.1	7	2	S78024
10	14	31.1	8	2	A42057
11	14	31.1	8	2	S66296
12	14	31.1	9	2	B39841
13	14	31.1	9	2	A39841
14	14	31.1	9	2	C57444
15	14	28.9	6	2	A46474
16	13	28.9	7	2	S08606
17	13	28.9	7	2	S42407
18	13	28.9	7	2	PT0520
19	13	28.9	9	2	PT0238
20	12	26.7	4	2	I38888
21	12	26.7	4	2	A35779
22	12	26.7	4	2	PT0712
23	12	26.7	5	2	S70154
24	12	26.7	7	2	PC2370
25	12	26.7	7	2	PN0649
26	12	26.7	7	2	S29735
27	12	26.7	8	2	XGHEU
28	12	26.7	8	2	T14906
29	12	26.7	8	2	B27867

ALIGNMENTS

30	12	26.7	8	2	H41978	callifmrfamide 8 -
31	12	26.7	8	2	A36887	r-cell receptor ga
32	12	26.7	9	2	T31612	hypothetical prote
33	12	26.7	9	2	JN0027	[phe-6]-mosact - s
34	12	26.7	9	2	S36850	ig heavy chain v r
35	12	26.7	9	2	PD0027	pev-tracykinin - p
36	11	24.4	4	2	J01273	neuropeptide Antho
37	11	24.4	5	2	JN0860	peptidyl-dipeptida
38	11	24.4	5	2	I40698	biotin B - Citroba
39	11	24.4	5	2	B37325	pap fibribial regul
40	11	24.4	6	2	B34835	dnaa protein - pse
41	11	24.4	7	2	B44787	callifmrfamide 11
42	11	24.4	7	2	I48086	DNA topoisomerase
43	11	24.4	8	2	E60588	sperm-activating p
44	11	24.4	8	2	G60588	sperm-activating p
45	11	24.4	9	1	AKQIM	locustamyoindhibiti

RESULT 1

S07205 litorin 2-Glu - Australian tree frog (Litoria aurea)

C:Species: Litoria aurea

C:Date: 12-Feb-1993 #sequence-revision 12-Mar-1993 #text-change 18-Aug-2000

C:Accession: S07205

R:Anastasi, A.; Montecucchi, P.; Angelucci, F.; Erspamer, V.; Endean, R.

Experientia 33, 1289, 1977

A:Title: Glu(OMe)(2)-litorin, the second bombesin-like peptide occurring in methanol

A:Reference number: S07205; PMID:78003546

A:Accession: S07205

A:Molecule type: protein

A:Residues: 1-9 <NA>

C:Superfamily: gastrin-releasing peptide

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.8% Score 17; DB 2; Length 9;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 1shf1 8

DB 5 VGHFM 9

RESULT 2

S07204 litorin I - Australian tree frog (Litoria aurea)

C:Species: Litoria aurea

C:Date: 12-Feb-1993 #sequence-revision 12-Mar-1993 #text-change 18-Aug-2000

C:Accession: S07204

R:Anastasi, A.; Erspamer, V.; Endean, R.

Experientia 31, 510-511, 1975

A:Title: Amino acid composition and sequence of litorin, a bombesin-like nonapeptide f

A:Reference number: S07204; PMID:75187011

A:Accession: S07204

A:Molecule type: protein

A:Residues: 1-9 <NA>

C:Superfamily: gastrin-releasing peptide

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.8% Score 17; DB 2; Length 9;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 1shf1 8

Db 5 VGHFM 9

RESULT 3

S07241
Iltorin - Rohde's leaf frog
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
C:Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C:Accession: S07241
R:Barra, D.; Falconieri, Erspamer, G.; Simmaco, M.; Bossa, F.; Melchiorri, P.; Erspamer, F.B.S. Lett. 182, 53-56, 1985
A:Title: Rohdei-iltorin: a new peptide from the skin of Phyllomedusa rohdei.
A:Reference number: S07241; MUID:85127560
A:Accession: S07241
A:Molecule type: protein
A:Residues: 1-9 <BAR>
C:Superfamily: gastrin-releasing peptide
C:Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 35.6%; Score 16; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0;

OY 6 hfl 8
||:
Db 7 HFM 9

RESULT 4

D48186
ARPAase R1 subunit - wood tobacco (fragment)
C:Species: Nicotiana sylvestris (wood tobacco)
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997
C:Accession: D48186
R:De Paeppe, R.; Forchioni, A.; Chetrit, P.; Vedel, F.
Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993
A:Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthase
A:Reference number: A48186; MUID:93317598
A:Accession: D48186
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9
A:Experimental source: pollen
A:Note: sequence extracted from NCBI backbone (NCBIP:134871)

Query Match 35.6%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0;

OY 2 vdlshf 7
|||:
Db 3 VDLAPY 8

RESULT 5

PC4131
Hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PC4131
R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A:Title: Sequencing and characterization of the downstream region of the genes encoding
Y for biosynthesis of heme d1.
A:Reference number: JC4552; MUID:96144254
A:Accession: PC4131
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-8 <RAW>
A:Cross-references: DDBJ:D50473; NID:q1217594
A:Note: this ORF is not annotated in GenBank entry PSENIIRC, release 113.0

Query Match 33.3%; Score 15; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0;

OY 3 dlsfl 8
|||:
Db 3 DLSRL 8

RESULT 6

JN0026
sperm-activating peptide SAP-b - sea urchin (Clypeaster japonicus)
N:Alternate names: [His-6]-mosact
C:Species: Clypeaster japonicus
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Aug-2000
C:Accession: JN0026; B60973
R:Suzuki, N.; Kurita, M.; Yoshino, K.; Kajima, H.; Nomura, K.; Yamaguchi, M.
Zool. Sci. 4, 649-656, 1987
A:Title: Purification and structure of mosact and its derivatives from the egg jelly
A:Reference number: JN0025
A:Accession: JN0026
A:Molecule type: protein
A:Residues: 1-9 <SUZ>
R:Itakao, T.; Yoshino, K.; Suzuki, N.; Shimonishi, Y.
Biomed. Environ. Mass Spectrom. 19, 705-712, 1990
A:Title: Analysis of post-translational modifications of proteins by accurate mass measurement
A:Reference number: A60973; MUID:91167743
A:Accession: B60973
A:Molecule type: protein
A:Residues: 1-9 <TAK>
C:Comment: SAP-b (mosact), one of several sperm activating peptides located in egg jelly
C:Comment: Forms with and without the bromohistidine moiety were purified separately.
C:Superfamily: unassigned animal peptides
C:Keywords: bromine
F:6/Modified site: bromohistidine (His) (partial) #status experimental

Query Match 33.3%; Score 15; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 dlsfl 8
|||:
Db 3 DSAHLI 8

RESULT 7

A58728
Serratwettin W2 - Serratia marcescens
C:Species: Serratia marcescens
C:Date: 10-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 12-Feb-1998
C:Accession: A58728
R:Matsuyama, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.
J. Bacteriol. 174, 1769-1776, 1992
A:Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent
A:Reference number: A58728; MUID:92193260
A:Accession: A58728
A:Status: unencoded polypeptide
A:Molecule type: protein
A:Residues: 1-5 <MAT>
A:Experimental source: strain NS 25
C:Comment: A surfactant lipopeptide promoting flagellum-independent surface translocation
C:Keywords: blocked amino end; blocked carboxyl end; D-amino acid; lipoprotein; unenc
F:1/Modified site: D-phenylalanine (Phe) #status experimental
F:4/Modified site: D-phenylalanine (Phe) #status experimental
F:1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Leu-11e) #status e

Query Match 31.1%; Score 14; DB 4; Length 5;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 lshfl 8
 | | |
 Db 1 LSTFI 5

RESULT 8
 S20446
 elastase - Pseudomonas aeruginosa
 C:Species: Pseudomonas aeruginosa
 C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
 C:Accession: S20446
 R:Kessler, E.; Safir, M.; Peretz, M.; Birstein, Y.
 FBS Lett. 299, 291-293, 1992
 A:Title: Identification of cleavage sites involved in proteolytic processing of Pseudom
 A:Reference number: S20446; MUID:92183956
 A:Accession: S20446
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <RES>

Query Match 31.1%; Score 14; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 avd1 4
 | | |
 Db 1 AADL 4

RESULT 9
 S78024
 ribosomal protein YML21, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)
 C:Species: Saccharomyces cerevisiae
 C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997
 C:Accession: S78024
 R:Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittma
 Eur. J. Biochem. 245, 449-456, 1997
 A:Title: Identification and characterization of the genes for mitochondrial ribosomal pr
 A:Reference number: S78018; MUID:97296414
 A:Accession: S78024
 A:Molecule type: protein
 A:Residues: 1-7 <KIT>
 C:Genetics:
 A:Genome: nuclear
 C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 31.1%; Score 14; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 lshfl 9
 | | |
 Db 2 LXMLK 7

RESULT 10
 A42057
 fibroblast growth factor receptor 1, secreted - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
 C:Accession: A42057
 R:Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.
 Mol. Cell. Biol. 12, 82-88, 1992
 A:Title: Differential splicing in the extracellular region of fibroblast growth factor r
 A:Reference number: A42057; MUID:92107200
 A:Accession: A42057
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-8 <MER>
 A:Cross-references: GB:M80363
 C:Keywords: growth factor receptor

Query Match 31.1%; Score 14; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 lshfl 8
 | | |
 Db 3 LTSFL 7

RESULT 11
 S66296
 Na⁺-transporting ATP synthase (EC 3.6.1.-) chain c - Acetobacterium woodii (fragment)
 N:Alternate names: ATPase chain c
 C:Species: Acetobacterium woodii
 C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
 C:Accession: S66296
 R:Reidlinger, J.; Mueller, V.
 Eur. J. Biochem. 223, 275-283, 1994
 A:Title: Purification of ATP synthase from Acetobacterium woodii and identification a
 A:Reference number: S45648; MUID:94307271
 A:Accession: S66296
 A:Molecule type: protein
 A:Residues: 1-8 <REI>
 A:Experimental source: DSM 1030
 C:Keywords: hydrolase

Query Match 31.1%; Score 14; DB 2; Length 8;
 Best Local Similarity 28.6%; Pred. No. 2.8e+05;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 dlsflk 9
 | | |
 Db 2 EILDFIK 8

RESULT 12
 B39841
 dextranucrase (EC 2.4.1.5) - Streptococcus sobrinus (fragment)
 C:Species: Streptococcus sobrinus
 C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 23-Jun-1993
 C:Accession: B39841
 R:Mooser, G.; Hefta, S.A.; Paxton, R.J.; Shively, J.E.; Lee, T.D.
 J. Biol. Chem. 266, 8916-8922, 1991
 A:Title: Isolation and sequence of an active-site peptide containing a catalytic aspa
 A:Reference number: A39841; MUID:91224988
 A:Accession: B39841
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <MOO>
 C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 31.1%; Score 14; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 avd 3
 | | |
 Db 7 AVD 9

RESULT 13
 A39841
 sucrase 3-glucosyltransferase (EC 2.4.1.-) - Streptococcus sobrinus (fragment)
 C:Species: Streptococcus sobrinus
 C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 21-Mar-1996

Search completed: July 3, 2002, 10:33:24
Job time: 178 sec

C:Accession: A39841
R:Mooser, G.; Hetta, S.A.; Paxton, R.J.; Shively, J.E.; Lee, T.D.
J. Biol. Chem. 266, 8916-8922, 1991
A:Title: Isolation and sequence of an active-site peptide containing a catalytic aspartate
A:Reference number: A39841; MUID:91224988
A:Accession: A39841
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <MOO>
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 31.1%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 avd 3
|||
Db 7 AVD 9

RESULT 14
C57444
neuropeptide Grb-AST B3 - two-spotted cricket
C:Species: Gryllus bimaculatus (two-spotted cricket)
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C:Accession: C57444
R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket
A:Reference number: A57444; MUID:95403341
A:Accession: C57444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <LOK>

Query Match 31.1%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 dls 5
|||
Db 4 DLS 6

RESULT 15
A46474
Fc epsilon RIIB - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C:Accession: A46474
R:Richards, M.L.; Katz, D.H.; Liu, F.T.
J. Immunol. 147, 1067-1074, 1991
A:Title: Complete genomic sequence of the murine low affinity Fc receptor for IgE. Demonstration of a novel exon
A:Reference number: A46474; MUID:91318149
A:Accession: A46474
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-6 <RIC>
A:Experimental source: BALB C, splenic B cells
A>Note: sequence extracted from NCBI backbone (NCBIP:45428)

Query Match 28.9%; Score 13; DB 2; Length 6;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 valsh 6
:| |
Db 1 MDTTH 5

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